

# 7



PCT/10

RAW SEQUENCE LISTING  
 PATENT APPLICATION: US/10/069,304

DATE: 08/30/2002  
 TIME: 15:33:16

Input Set : A:\Sequence Listing.txt  
 Output Set: N:\CRF4\08302002\J069304.raw

see p.6

C--> 4 <110> APPLICANT: GORING, Daphne R. et al.  
 6 <120> TITLE OF INVENTION: PROLINE-RICH EXTENSIN-LIKE RECEPTOR KINASES  
 8 <130> FILE REFERENCE: P 25,762 USA  
 10 <140> CURRENT APPLICATION NUMBER: US 10/069,304  
 11 <141> CURRENT FILING DATE: 2002-08-06  
 13 <150> PRIOR APPLICATION NUMBER: PCT/CA00/00966  
 14 <151> PRIOR FILING DATE: 2000-08-18  
 16 <150> PRIOR APPLICATION NUMBER: US 60/149,466  
 17 <151> PRIOR FILING DATE: 1999-08-19  
 19 <150> PRIOR APPLICATION NUMBER: US 60/159,122  
 20 <151> PRIOR FILING DATE: 1999-10-13  
 22 <160> NUMBER OF SEQ ID NOS: 27  
 24 <170> SOFTWARE: PatentIn Ver. 2.1  
 26 <210> SEQ ID NO: 1  
 27 <211> LENGTH: 1944  
 28 <212> TYPE: DNA  
 29 <213> ORGANISM: Brassica napus  
 31 <220> FEATURE:  
 32 <221> NAME/KEY: CDS  
 33 <222> LOCATION: (1)..(1944)  
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 37 Met Ser Ser Ala Pro Ser Pro Gly Thr Gly Ser Pro Pro Ser Pro Pro  
 38 1 5 10 15  
 40 tca aac tcc aca acc acc act cct cct cca gct tcc gct cct cct ccc 96  
 41 Ser Asn Ser Thr Thr Thr Thr Pro Pro Pro Ala Ser Ala Pro Pro Pro  
 42 20 25 30  
 44 acc aca cct tct tct cct ccg ccg cca tcc act att ccg aca tct cct 144  
 45 Thr Thr Pro Ser Ser Pro Pro Pro Pro Ser Thr Ile Pro Thr Ser Pro  
 46 35 40 45  
 48 cct cct tct tct cgc tct aca cct tct gct cct cct cca tct cca cca 192  
 49 Pro Pro Ser Ser Arg Ser Thr Pro Ser Ala Pro Pro Pro Ser Pro Pro  
 50 50 55 60  
 52 act cca tct acg ccg gga tct cca cct cct ctt cct cag ccg tct cca 240  
 53 Thr Pro Ser Thr Pro Gly Ser Pro Pro Pro Leu Pro Gln Pro Ser Pro  
 54 65 70 75 80  
 56 ccc gct cca act acg ccc gga tct cca ccc gca cct gtt act cct cct 288  
 57 Pro Ala Pro Thr Thr Pro Gly Ser Pro Pro Ala Pro Val Thr Pro Pro  
 58 85 90 95  
 60 act cga aac cct cca cct tca gtc cca gga cca ccg tcc aat cct tca 336  
 61 Thr Arg Asn Pro Pro Pro Ser Val Pro Gly Pro Pro Ser Asn Pro Ser  
 62 100 105 110  
 64 cgc gaa gga gga tct cct cga cct cca tct tct ccc tcg ccg ccg tct 384

ENTERED

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65	Arg	Glu	Gly	Gly	Ser	Pro	Arg	Pro	Pro	Ser	Ser	Pro	Ser	Pro	Pro	Ser	
66			115					120				125					
68	cct	tct	tcc	gac	ggt	tta	tca	aca	gga	gtg	gtg	gtg	gga	atc	gcc	atc	432
69	Pro	Ser	Ser	Asp	Gly	Leu	Ser	Thr	Gly	Val	Val	Val	Gly	Ile	Ala	Ile	
70			130					135				140					
72	gga	gga	gtc	gct	ctg	ctt	gtg	ata	gtg	act	ctg	att	tgt	ctc	ctc	tgt	480
73	Gly	Gly	Val	Ala	Leu	Leu	Val	Ile	Val	Thr	Leu	Ile	Cys	Leu	Leu	Cys	
74	145					150					155					160	
76	aag	aag	aaa	cga	cgg	aga	gac	gaa	gaa	gat	gct	tac	tat	gtt	cct	ccg	528
77	Lys	Lys	Lys	Arg	Arg	Arg	Asp	Glu	Glu	Asp	Ala	Tyr	Tyr	Val	Pro	Pro	
78					165					170					175		
80	cca	cct	cct	cct	ggt	ccc	aaa	gcc	gga	gga	cct	tac	ggt	gga	cag	cag	576
81	Pro	Pro	Pro	Pro	Gly	Pro	Lys	Ala	Gly	Gly	Pro	Tyr	Gly	Gly	Gln	Gln	
82				180					185					190			
84	caa	caa	tgg	cgg	caa	caa	aac	gca	aca	cca	ccg	tca	gat	cat	gtc	gtg	624
85	Gln	Gln	Trp	Arg	Gln	Gln	Asn	Ala	Thr	Pro	Pro	Ser	Asp	His	Val	Val	
86			195					200				205					
88	acg	tca	cta	cca	cca	cca	cct	aag	gct	cca	tct	cca	cca	cgg	caa	cct	672
89	Thr	Ser	Leu	Pro	Pro	Pro	Pro	Lys	Ala	Pro	Ser	Pro	Pro	Arg	Gln	Pro	
90			210				215					220					
92	cct	cca	cct	cca	cca	ccg	cct	ttc	atg	agc	agc	agc	ggc	ggc	tcc	gac	720
93	Pro	Pro	Pro	Pro	Pro	Pro	Pro	Phe	Met	Ser	Ser	Ser	Gly	Gly	Ser	Asp	
94	225				230					235					240		
96	tac	tcg	gac	cgt	cca	ggt	ctt	cct	cca	ccg	tct	cca	ggg	ctt	gtg	tta	768
97	Tyr	Ser	Asp	Arg	Pro	Val	Leu	Pro	Pro	Pro	Ser	Pro	Gly	Leu	Val	Leu	
98				245						250				255			
100	ggc	ttc	tcc	aaa	agc	act	ttc	aca	tac	gag	gag	cta	gct	aga	gcc	acc	816
101	Gly	Phe	Ser	Lys	Ser	Thr	Phe	Thr	Tyr	Glu	Glu	Leu	Ala	Arg	Ala	Thr	
102				260					265					270			
104	aat	ggt	ttc	tcc	gag	gcg	aac	ttg	tta	gga	caa	ggc	ggg	ttc	ggt	tac	864
105	Asn	Gly	Phe	Ser	Glu	Ala	Asn	Leu	Leu	Gly	Gln	Gly	Gly	Phe	Gly	Tyr	
106			275					280					285				
108	gtg	cac	aaa	ggt	gtg	ttg	cct	agt	ggg	aaa	gaa	gtt	gct	gtg	aag	cag	912
109	Val	His	Lys	Gly	Val	Leu	Pro	Ser	Gly	Lys	Glu	Val	Ala	Val	Lys	Gln	
110			290				295					300					
112	ttg	aaa	gtt	ggg	agt	ggt	cag	gga	gag	agg	gag	ttt	cag	gca	gag	gtt	960
113	Leu	Lys	Val	Gly	Ser	Gly	Gln	Gly	Glu	Arg	Glu	Phe	Gln	Ala	Glu	Val	
114	305					310					315				320		
116	gag	atc	atc	agc	aga	gtt	cac	cac	agg	cat	ctg	gtg	tct	ctt	gtt	ggt	1008
117	Glu	Ile	Ile	Ser	Arg	Val	His	His	Arg	His	Leu	Val	Ser	Leu	Val	Gly	
118				325						330				335			
120	tat	tgc	atc	gcc	ggt	gcc	aaa	aga	ttg	ctt	gtc	tat	gag	ttt	gtt	cct	1056
121	Tyr	Cys	Ile	Ala	Gly	Ala	Lys	Arg	Leu	Leu	Val	Tyr	Glu	Phe	Val	Pro	
122				340					345					350			
124	aac	aac	aat	ctc	gag	ctt	cac	ctc	cat	ggc	gag	gga	cgg	cct	aca	atg	1104
125	Asn	Asn	Asn	Leu	Glu	Leu	His	Leu	His	Gly	Glu	Gly	Arg	Pro	Thr	Met	
126			355					360				365					
128	gaa	tgg	agc	acc	aga	ttg	aag	att	gct	ctt	gga	tct	gct	aaa	gga	ctt	1152
129	Glu	Trp	Ser	Thr	Arg	Leu	Lys	Ile	Ala	Leu	Gly	Ser	Ala	Lys	Gly	Leu	

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130	370	375	380	
132	tct tat ctt cat gaa gat tgc aat cct aaa atc att cac cgt gat atc	1200		
133	Ser Tyr Leu His Glu Asp Cys Asn Pro Lys Ile Ile His Arg Asp Ile			
134	385 390 395 400			
136	aag gct tca aac ata ttg ata gat ttc aag ttt gaa gct aag gtt gct	1248		
137	Lys Ala Ser Asn Ile Leu Ile Asp Phe Lys Phe Glu Ala Lys Val Ala			
138	405 410 415			
140	gat ttt ggt ctt gct aag att gct tct gat aca aac acg cat gta tca	1296		
141	Asp Phe Gly Leu Ala Lys Ile Ala Ser Asp Thr Asn Thr His Val Ser			
142	420 425 430			
144	aca cgt gtg atg gga acc ttt ggg tac ttg gct ccg gaa tac gct gca	1344		
145	Thr Arg Val Met Gly Thr Phe Gly Tyr Leu Ala Pro Glu Tyr Ala Ala			
146	435 440 445			
148	agc gga aag ctc acg gag aag tct gac gtt ttc tca ttt ggc gtt gtg	1392		
149	Ser Gly Lys Leu Thr Glu Lys Ser Asp Val Phe Ser Phe Gly Val Val			
150	450 455 460			
152	ctt ttg gag ctc att act gga cgt cga ccc gtt gat gcc aac aat gtc	1440		
153	Leu Leu Glu Leu Ile Thr Gly Arg Arg Pro Val Asp Ala Asn Asn Val			
154	465 470 475 480			
156	tat gta gat gac agc tta gtt gac tgg gca cga cca ttg ctt aac cga	1488		
157	Tyr Val Asp Asp Ser Leu Val Asp Trp Ala Arg Pro Leu Leu Asn Arg			
158	485 490 495			
160	gca tct gag caa gga gac ttt gag ggt tta gct gat gca aag atg aat	1536		
161	Ala Ser Glu Gln Gly Asp Phe Glu Gly Leu Ala Asp Ala Lys Met Asn			
162	500 505 510			
164	aat ggg tat gac aga gag gag atg gct cgc atg gtt gct tgt gct gcg	1584		
165	Asn Gly Tyr Asp Arg Glu Glu Met Ala Arg Met Val Ala Cys Ala Ala			
166	515 520 525			
168	gct tgt gtt cgc cat tca gct cgc cgc aga cct cgc atg agc cag att	1632		
169	Ala Cys Val Arg His Ser Ala Arg Arg Arg Pro Arg Met Ser Gln Ile			
170	530 535 540			
172	gtg cgt gcg tta gaa gga aat gta tca ctg tca gat ctt aac gaa ggg	1680		
173	Val Arg Ala Leu Glu Gly Asn Val Ser Leu Ser Asp Leu Asn Glu Gly			
174	545 550 555 560			
176	atg aga cca ggt caa agc aat gta tac agc tca tac gga gga agc acc	1728		
177	Met Arg Pro Gly Gln Ser Asn Val Tyr Ser Ser Tyr Gly Gly Ser Thr			
178	565 570 575			
180	gat tat gac tcg agc cag tac aat gaa gac atg aag aag ttt agg aaa	1776		
181	Asp Tyr Asp Ser Ser Gln Tyr Asn Glu Asp Met Lys Lys Phe Arg Lys			
182	580 585 590			
183	atg gca ctt gga act caa gag tac aac gcc acg ggt gag tac agt aat	1824		
184	Met Ala Leu Gly Thr Gln Glu Tyr Asn Ala Thr Gly Glu Tyr Ser Asn			
185	595 600 605			
187	ccg acc agt gac tat gga ctg tac ccg tct ggt tca agc agc gag ggc	1872		
188	Pro Thr Ser Asp Tyr Gly Leu Tyr Pro Ser Gly Ser Ser Ser Glu Gly			
189	610 615 620			
191	caa acc aca cgc gaa atg gag atg ggg aag att aag aga acc ggt cag	1920		
192	Gln Thr Thr Arg Glu Met Glu Met Gly Lys Ile Lys Arg Thr Gly Gln			
193	625 630 635 640			

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197 645
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201 <211> LENGTH: 647
202 <212> TYPE: PRT
203 <213> ORGANISM: Brassica napus
205 <400> SEQUENCE: 2
206 Met Ser Ser Ala Pro Ser Pro Gly Thr Gly Ser Pro Pro Ser Pro Pro
207 1 5 10 15
208 Ser Asn Ser Thr Thr Thr Thr Pro Pro Pro Ala Ser Ala Pro Pro Pro
209 20 25 30
210 Thr Thr Pro Ser Ser Pro Pro Pro Pro Ser Thr Ile Pro Thr Ser Pro
211 35 40 45
212 Pro Pro Ser Ser Arg Ser Thr Pro Ser Ala Pro Pro Pro Ser Pro Pro
213 50 55 60
214 Thr Pro Ser Thr Pro Gly Ser Pro Pro Pro Leu Pro Gln Pro Ser Pro
215 65 70 75 80
216 Pro Ala Pro Thr Thr Pro Gly Ser Pro Pro Ala Pro Val Thr Pro Pro
217 85 90 95
218 Thr Arg Asn Pro Pro Pro Ser Val Pro Gly Pro Pro Ser Asn Pro Ser
219 100 105 110
220 Arg Glu Gly Gly Ser Pro Arg Pro Pro Ser Ser Pro Ser Pro Pro Ser
221 115 120 125
222 Pro Ser Ser Asp Gly Leu Ser Thr Gly Val Val Val Gly Ile Ala Ile
223 130 135 140
224 Gly Gly Val Ala Leu Leu Val Ile Val Thr Leu Ile Cys Leu Leu Cys
225 145 150 155 160
226 Lys Lys Lys Arg Arg Arg Asp Glu Glu Asp Ala Tyr Tyr Val Pro Pro
227 165 170 175
228 Pro Pro Pro Pro Gly Pro Lys Ala Gly Gly Pro Tyr Gly Gly Gln Gln
229 180 185 190
230 Gln Gln Trp Arg Gln Gln Asn Ala Thr Pro Pro Ser Asp His Val Val
231 195 200 205
232 Thr Ser Leu Pro Pro Pro Pro Lys Ala Pro Ser Pro Pro Arg Gln Pro
233 210 215 220
234 Pro Pro Pro Pro Pro Pro Pro Phe Met Ser Ser Ser Gly Gly Ser Asp
235 225 230 235 240
236 Tyr Ser Asp Arg Pro Val Leu Pro Pro Pro Ser Pro Gly Leu Val Leu
237 245 250 255
238 Gly Phe Ser Lys Ser Thr Phe Thr Tyr Glu Glu Leu Ala Arg Ala Thr
239 260 265 270
240 Asn Gly Phe Ser Glu Ala Asn Leu Leu Gly Gln Gly Gly Phe Gly Tyr
241 275 280 285
242 Val His Lys Gly Val Leu Pro Ser Gly Lys Glu Val Ala Val Lys Gln
243 290 295 300
244 Leu Lys Val Gly Ser Gly Gln Gly Glu Arg Glu Phe Gln Ala Glu Val
245 305 310 315 320
246 Glu Ile Ile Ser Arg Val His His Arg His Leu Val Ser Leu Val Gly

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247          325          330          335
248 Tyr Cys Ile Ala Gly Ala Lys Arg Leu Leu Val Tyr Glu Phe Val Pro
249          340          345          350
250 Asn Asn Asn Leu Glu Leu His Leu His Gly Glu Gly Arg Pro Thr Met
251          355          360          365
252 Glu Trp Ser Thr Arg Leu Lys Ile Ala Leu Gly Ser Ala Lys Gly Leu
253          370          375          380
254 Ser Tyr Leu His Glu Asp Cys Asn Pro Lys Ile Ile His Arg Asp Ile
255 385          390          395          400
256 Lys Ala Ser Asn Ile Leu Ile Asp Phe Lys Phe Glu Ala Lys Val Ala
257          405          410          415
258 Asp Phe Gly Leu Ala Lys Ile Ala Ser Asp Thr Asn Thr His Val Ser
259          420          425          430
260 Thr Arg Val Met Gly Thr Phe Gly Tyr Leu Ala Pro Glu Tyr Ala Ala
261          435          440          445
262 Ser Gly Lys Leu Thr Glu Lys Ser Asp Val Phe Ser Phe Gly Val Val
263          450          455          460
264 Leu Leu Glu Leu Ile Thr Gly Arg Arg Pro Val Asp Ala Asn Asn Val
265 465          470          475          480
266 Tyr Val Asp Asp Ser Leu Val Asp Trp Ala Arg Pro Leu Leu Asn Arg
267          485          490          495
268 Ala Ser Glu Gln Gly Asp Phe Glu Gly Leu Ala Asp Ala Lys Met Asn
269          500          505          510
270 Asn Gly Tyr Asp Arg Glu Glu Met Ala Arg Met Val Ala Cys Ala Ala
271          515          520          525
272 Ala Cys Val Arg His Ser Ala Arg Arg Arg Pro Arg Met Ser Gln Ile
273          530          535          540
274 Val Arg Ala Leu Glu Gly Asn Val Ser Leu Ser Asp Leu Asn Glu Gly
275 545          550          555          560
276 Met Arg Pro Gly Gln Ser Asn Val Tyr Ser Ser Tyr Gly Gly Ser Thr
277          565          570          575
278 Asp Tyr Asp Ser Ser Gln Tyr Asn Glu Asp Met Lys Lys Phe Arg Lys
279          580          585          590
280 Met Ala Leu Gly Thr Gln Glu Tyr Asn Ala Thr Gly Glu Tyr Ser Asn
281          595          600          605
282 Pro Thr Ser Asp Tyr Gly Leu Tyr Pro Ser Gly Ser Ser Ser Glu Gly
283          610          615          620
284 Gln Thr Thr Arg Glu Met Glu Met Gly Lys Ile Lys Arg Thr Gly Gln
285 625          630          635          640
286 Gly Tyr Ser Gly Pro Ser Leu
287          645
290 <210> SEQ ID NO: 3
291 <211> LENGTH: 2189
292 <212> TYPE: DNA
293 <213> ORGANISM: Brassica napus
297 <220> FEATURE:
298 <221> NAME/KEY: CDS
299 <222> LOCATION: (1)..(2189)
300 <223> OTHER INFORMATION:

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Please Note:

Use of n and/or Xaa have been detected in the Sequence Listing. Please review the Sequence Listing to ensure that a corresponding explanation is presented in the <220> to <223> fields of each sequence which presents at least one n or Xaa.

Seq#:18; N Pos. 3,12,15,18,21,22,25

Seq#:19; Xaa Pos. 7

Seq#:20; N Pos. 3,6,8,9,15,18,21,22

Seq#:23; N Pos. 2,3,5,6,9,12,14,15,18,21